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Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu 50 55 60

Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val Met Phe Thr Ala 65 70 75 80

Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln Ala Asp Glu Glu 85 90 95

Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Thr Asn 100 105 110

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Gln Met Leu Asn Met Asn Ser Ala Pro Thr Phe Ile Asn Phe Pro Ala 130 135 140

Lys Gly Lys Pro Lys Arg Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly 145 150 155 160

Phe Ser Ala Glu Gln Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val 165 170 175

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Gly Leu Leu Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser 195 200 205

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Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His Ile Val 260

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The His Gly His Val Asn Tyr 255

The His Ile Val 260

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The Wal Ala Gl

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Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys Ile Met Cys Val 290 295 300

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Ser Leu Thr His Leu Thr Ala Leu His Leu Ser Asp Asn Ser Leu Ser 50 55 60

Arg Ile Pro Ser Asp Ile Ala Lys Leu His Asn Leu Val Tyr Leu Asp 65 70 75 80

Leu Ser Ser Asn Lys Ile Arg Ser Leu Pro Ala Glu Leu Gly Asn Met 85 90 95

Val Ser Leu Arg Glu Leu His Leu Asn Asn Asn Leu Leu Arg Val Leu 100 105 110

Pro Phe Glu Leu Gly Lys Leu Phe Gln Leu Gln Thr Leu Gly Leu Lys 115 120 125

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Gln Ala Glu Leu Ser Arg Thr Gly Arg Ser Arg Glu Val Leu Glu Leu 50 55 60

Gly Gln Val Leu Asp Thr Gly Lys Arg Lys Arg His Val Pro Tyr Ser 65 70 75 80

Val Ser Glu Thr Arg Leu Glu Glu Ala Leu Glu Asn Leu Cys Glu Arg 85 90 95

Ile Leu Asp Tyr Ser Val His Ala Glu Arg Lys Gly Ser Leu Arg Tyr 100 105 110

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Lys Gly Val Lys Val Asp Leu Gly Ile Pro Leu Glu Leu Trp Asp Glu 130 135 140

Pro Ser Val Glu Val Thr Tyr Leu Lys Lys Gln Cys Glu Thr Met Leu 145 150 155 160

Glu Glu Phe Glu Asp Ile Val Gly Asp Trp Tyr Phe His His Gln Glu 165 170 175

Gln Pro Leu Gln Asn Phe Leu Cys Glu Gly His Val Leu Pro Ala Ala 180 185 190

Glu Thr Ala Cys Leu Gln Glu Thr Trp Thr Gly Lys Glu Ile Thr Asp 195 200 205

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Cys Asn Met Thr Val Leu Ser Met Leu Pro Thr Leu Arg Glu Ala Leu 65 70 75

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- Pro Ser Asn Lys Leu Glu Ile Trp Glu Asp Leu Lys Ile Ile Ser Phe 100 105 110
- Thr Arg Ser Thr Val Ala Val Tyr Ser Thr Cys Met Leu Val Val Leu
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- Leu Arg Val Gln Leu Asn Ile Ile Gly Gly Tyr Ile Tyr Leu Asp Asn 130 135 140
- Ala Ala Val Gly Lys Asn Gly Thr Thr Ile Leu Ala Pro Pro Asp Val 145 150 155 160
- Gln Gln Gln Tyr Leu Ser Ser Ile Gln His Leu Leu Gly Asp Gly Leu
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- Thr Glu Leu Ile Thr Val Ile Lys Gln Ala Val Gln Lys Val Leu Gly
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- Ser Val Ser Leu Lys His Ser Leu Ser Leu Leu Asp Leu Glu Gln Lys
 195 200 205
- Leu Lys Glu Ile Arg Asn Leu Val Glu Gln His Lys Ser Ser Ser Trp
 210 215 220
- Ile Asn Lys Asp Gly Ser Lys Pro Leu Leu Cys His Tyr Met Met Pro 225 230 235 240
- Asp Glu Glu Thr Pro Leu Ala Val Gln Ala Cys Gly Leu Ser Pro Arg 245 250 255
- Asp Ile Thr Thr Ile Lys Leu Leu Asn Glu Thr Arg Asp Met Leu Glu 260 265 270
- Ser Pro Asp Phe Ser Thr Val Leu Asn Thr Cys Leu Asn Arg Gly Phe 275 280 285
- Ser Arg Leu Leu Asp Asn Met Ala Glu Phe Phe Arg Pro Thr Glu Gln 290 295 300
- Asp Leu Gln His Gly Asn Ser Met Asn Ser Leu Ser Ser Val Ser Leu 305 310 315 320
- Pro Leu Ala Lys Ile Ile Pro Ile Val Asn Gly Gln Ile His Ser Val 325 330 335
- Cys Ser Glu Thr Pro Ser His Phe Val Gln Asp Leu Leu Thr Met Glu 340 345 350
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Glu Leu Ser Glu Leu Tyr Ser Tyr Thr Glu Gly Pro Glu Phe Leu Met 85 90 95

Asn Arg Lys Cys Phe Glu Glu Asp Phe Arg Ile His Val Thr Asp Lys 100 105 110

Lys Trp Thr Glu Leu Asp Thr Asn Gln His Arg Thr His Ala Met Arg

Leu Leu Asp Gly Leu Glu Val Thr Ala Arg Glu Lys Arg Leu Lys Val

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Ser Glu Ala Glu Val Gln Ser Trp Met Arg Tyr Asn Ile Phe Leu Leu 165 170 175

Leu Glu Val Gly Thr Phe Asn Ala Leu Val Glu Leu Leu Asn Met Glu 180 185 190

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Ser Leu Ala Asp Ser Thr Asp Leu Arg Val Leu Leu Asn Ile Met Tyr 210 215 220

Leu Ile Val Glu Thr Val His Gln Glu Cys Glu Gly Asp Lys Ala Glu 225 230 235 240

Trp Arg Thr Met Arg Gln Thr Phe Arg Ala Glu Leu Gly Ser Pro Leu 245 250 255

Tyr Asn Asn Glu Pro Phe Ala Ile Met Leu Phe Gly Met Val Thr Lys 260 265 270

Phe Cys Ser Gly His Ala Pro His Phe Pro Met Lys Lys Val Leu Leu 275 280 280

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- Pro Glu Asp Ser Ile Lys Val Ile Arg Asn Met Arg Ala Ala Ser Pro 325 330 335
- Pro Ala Ser Ala Ser Asp Leu Ile Glu Gln Gln Gln Lys Arg Gly Arg 340 345 350
- Arg Glu His Lys Ala Leu Ile Lys Gln Asp Asn Leu Asp Ala Phe Asn 355 360 365
- Asn Asp Asp Asp Asn Ser Leu Glu Gly Glu Thr Phe Pro Leu Glu Arg 385 390 395 400
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- Thr Cys Pro Lys Gly Leu Pro Trp Ala Pro Lys Val Arg Glu Lys Asp 420 425 430
- Ile Glu Met Phe Leu Glu Ser Ser Arg Ser Lys Phe Ile Gly Tyr Thr
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- Glu Ser Ile Lys Thr Leu Lys Gln His Lys Tyr Thr Ser Ile Ala Glu 465 470 475 480
- Val Gln Ala Gln Met Glu Glu Glu Tyr Leu Arg Ser Pro Leu Ser Gly
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- Leu Ala Ala Ala Pro Thr Ser Lys Ala Lys Thr Asp Ser Ile Asn Ile 530 535 540
- Leu Ala Asp Val Leu Pro Glu Glu Met Pro Thr Thr Val Leu Gln Ser 555 550 560
- Met Lys Leu Gly Val Asp Val Asn Arg His Lys Glu Val Ile Val Lys 565 570 575
- Ala Ile Ser Ala Val Leu Leu Leu Leu Leu Lys His Phe Lys Leu Asn 580 585 590

His Val Tyr Gln Phe Glu Tyr Met Ala Gln His Leu Val Phe Ala Asn 600

- Cys Ile Pro Leu Ile Leu Lys Phe Phe Asn Gln Asn Ile Met Ser Tyr
- Ile Thr Ala Lys Asn Ser Ile Ser Val Leu Asp Tyr Pro His Cys Val 635
- Val His Glu Leu Pro Glu Leu Thr Ala Glu Ser Leu Glu Ala Gly Asp 645
- Ser Asn Gln Phe Cys Trp Arg Asn Leu Phe Ser Cys Ile Asn Leu Leu 660 665
- Arg Ile Leu Asn Lys Leu Thr Lys Trp Lys His Ser Arg Thr Met Met 680
- Leu Val Val Phe Lys Ser Ala Pro Ile Leu Lys Arg Ala Leu Lys Val 695
- Lys Gln Ala Met Met Gln Leu Tyr Val Leu Lys Leu Lys Val Gln 710 715
- Thr Lys Tyr Leu Gly Arg Gln Trp Arg Lys Ser Asn Met Lys Thr Met 730
- Ser Ala Ile Tyr Gln Lys Val Arg His Arg Leu Asn Asp Asp Trp Ala 745 750
- Tyr Gly Asn Asp Leu Asp Ala Arg Pro Trp Asp Phe Gln Ala Glu Glu 760
- Cys Ala Leu Arg Ala Asn Ile Glu Arg Phe Asn Ala Arg Arg Tyr Asp
- Arg Ala His Ser Asn Pro Asp Phe Leu Pro Val Asp Asn Cys Leu Gln 790 795
- Ser Val Leu Gly Gln Arg Val Asp Leu Pro Glu Asp Phe Gln Met Asn 805 810
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Ser Arg Val Asp Gln Arg His Arg Ala Ser Gln Leu Arg Lys Gln Lys
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Lys Glu Ala Val Leu Ala Glu Lys Arg Gln Leu Gly Gly Lys Asp Gly
Pro Pro His Gln Val Leu Val Val Pro Leu His Ser Arg Ile Ser Leu
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Pro Glu Ala Met Gln Leu Leu Gln Asp Arg Asp Thr Gly Thr Val His
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2671

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Leu Lys His Leu Trp Phe Phe Thr Ser Ala Arg Pro Gly Asp Leu His 130 135 140

- Val Val Leu Asp Met Ala Lys Val Ala Asp Thr Ile Leu Phe Leu Leu 145 150 155 160
- Asp Pro Leu Glu Gly Trp Asp Ser Thr Arg Asp Tyr Cys Leu Ser Cys 165 170 175
- Leu Phe Ala Gln Gly Leu Pro Thr Tyr Thr Leu Ala Val Gln Gly Ile 180 185 190
- Ser Gly Leu Pro Leu Lys Lys Gln Ile Asp Thr Arg Lys Lys Leu Ser 195 200 205
- Lys Ala Val Glu Lys Arg Phe Pro His Asp Lys Leu Leu Leu Leu Asp 210 215 220
- Thr Gln Gln Glu Ala Gly Met Leu Leu Arg Gln Leu Ala Asn Gln Lys 225 230 235 240
- Gln Gln His Leu Ala Phe Arg Asp Arg Arg Ala Tyr Leu Phe Ala His 245 250 255
- Ala Val Asp Phe Val Pro Ser Glu Glu Asn Asn Leu Val Gly Thr Leu 260 265 270
- Lys Ile Ser Gly Tyr Val Arg Gly Gln Thr Leu Asn Val Asn Arg Leu 275 280 285
- Leu His Ile Val Gly Tyr Gly Asp Leu Pro Asp Glu Gln Ile Asp Ala 290 295 300
- Pro Gly Asp Pro Phe Pro Leu Asn Pro Arg Gly Ile Lys Pro Gln Lys 305 310 315 320
- Asp Pro Asp Met Ala Met Glu Ile Cys Ala Thr Asp Ala Val Asp Asp 325 330 335
- Met Glu Glu Gly Leu Lys Val Leu Met Lys Ala Asp Pro Gly Arg Gln 340 345 350
- Glu Ser Leu Gln Ala Glu Val Ile Pro Asp Pro Met Glu Gly Glu Gln 355 360 365
- Thr Trp Pro Thr Glu Glu Glu Leu Ser Glu Ala Lys Asp Phe Leu Lys 370 375 380
- Glu Ser Ser Lys Val Val Lys Lys Val Pro Lys Gly Thr Ser Ser Tyr 385 390 395
- Gln Ala Glu Trp Ile Leu Asp Gly Gly Ser Gln Ser Gly Gly Glu Gly
 405 410 415
- Asp Glu Tyr Glu Tyr Asp Asp Met Glu His Glu Asp Phe Met Glu Glu 420 425 430
- Glu Ser Gln Asp Glu Ser Ser Glu Glu Glu Glu Glu Tyr Glu Thr Met

435

440

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445

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- Glu Glu Met Phe Pro Asp Glu Val Asp Thr Pro Arg Asp Val Ala Ala 490
- Arg Ile Arg Phe Gln Lys Tyr Arg Gly Leu Lys Ser Phe Arg Thr Ser 505
- Pro Trp Asp Pro Lys Glu Asn Leu Pro Gln Asp Tyr Ala Arg Ile Phe
- Gln Phe Gln Asn Phe Thr Asn Thr Arg Lys Ser Ile Phe Lys Glu Val 535
- Glu Glu Lys Glu Val Glu Gly Ala Glu Val Gly Trp Tyr Val Thr Leu 550
- His Val Ser Glu Val Pro Val Ser Val Val Glu Cys Phe Arg Gln Gly 565
- Thr Pro Leu Ile Ala Phe Ser Leu Leu Pro His Glu Gln Lys Met Ser 585
- Val Leu Asn Met Val Val Arg Arg Asp Pro Gly Asn Thr Glu Pro Val
- Lys Ala Lys Glu Glu Leu Ile Phe His Cys Gly Phe Arg Arg Phe Arg 615
- Ala Ser Pro Leu Phe Ser Gln His Thr Ala Ala Asp Lys His Lys Leu 630
- Gln Arg Phe Leu Thr Ala Asp Met Ala Leu Val Ala Thr Val Tyr Ala 645
- Pro Ile Thr Phe Pro Pro Ala Ser Val Leu Leu Phe Lys Gln Lys Ser
- Asn Gly Met His Ser Leu Ile Ala Thr Gly His Leu Met Ser Val Asp 680
- Pro Asp Arg Met Val Ile Lys Arg Val Val Leu Ser Gly His Pro Phe 695
- Lys Ile Phe Thr Lys Met Ala Val Val Arg Tyr Met Phe Phe Asn Arg
- Glu Asp Val Leu Trp Phe Lys Pro Val Glu Leu Arg Thr Lys Trp Gly 730
- Arg Arg Gly His Ile Lys Glu Pro Leu Gly Thr His Gly His Met Lys
- Cys Ser Phe Asp Gly Lys Leu Lys Ser Gln Asp Thr Val Leu Met Asn

755

760

765

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Phe Gly Ala Gly Thr Glu Ser Tyr Phe Ser Leu Leu Arg Phe Leu Leu 35 40 45

Leu Leu Asn Val Leu Ala Ser Val Leu Met Ala Cys Met Thr Leu Leu
50 55 60

Pro Thr Trp Leu Gly Gly Ala Pro Pro Gly Pro Pro Gly Pro Asp Ile
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Ser Ser Pro Cys Gly Ser Tyr Asn Pro His Ser Gln Gly Leu Val Thr 85 90 95

Phe Ala Thr Gln Leu Phe Asn Leu Leu Ser Gly Glu Gly Tyr Leu Glu
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Trp Ser Pro Leu Phe Tyr Gly Phe Tyr Thr Pro Arg Pro Arg Leu Ala 115 120 125

Val Thr Tyr Leu Cys Trp Ala Phe Ala Val Gly Leu Ile Cys Leu Leu 130 135 140

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Ser Val Pro Leu Tyr Leu Ile Tyr Pro Ser Val Glu Asn Val Arg Thr 50 55 60

Ser Leu Glu Gly Tyr Pro Ala Gly Gly Ser Leu Pro Tyr Ser Ile Gln 65 70 75 80

Thr Ala Glu Lys Gln Asn Trp Leu His Ser Tyr Phe His Lys Trp Ser 85 90 95

Ala Glu Thr Ser Gly Arg Ser Asn Ala Met Pro His Ile Lys Thr Tyr
100 105 110

Met Arg Pro Ser Pro Asp Phe Ser Lys Ile Ala Trp Phe Leu Val Thr 115 120 125

Ser Ala Asn Leu Ser Lys Ala Ala Trp Gly Ala Leu Glu Lys Asn Gly 130 135 140

Thr Gln Leu Met Ile Arg Ser Tyr Glu Leu Gly Val Leu Phe Leu Pro 145 150 155 160

Ser Ala Phe Gly Leu Asp Ser Phe Lys Val Lys Gln Lys Phe Phe Ala 165 170 175

Gly Ser Gln Glu Pro Met Ala Thr Phe Pro Val Pro Tyr Asp Leu Pro 180 185 190

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- Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile 65 70 75 80
- Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp
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- Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp 100 105 110
- Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp 115 120 125
- Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys 130 135 140
- Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe 145 150 155 160
- Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg 165 170 175
- Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu 180 185 190
- Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr 195 200 205
- Ala Arg Tyr Ser Lys Glu Glu Met Asp Asp Met Asp Arg Asp Leu 210 215 220
- Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro 225 230 235 240
- Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln 245 250 255
- Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp 260 265 270
- Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr 275 280 285
- Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala 290 295 300

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Val Asp Ser Leu Gly Pro Leu Glu Lys Gly Gln Val Lys Asn Glu Ala 130 135 140

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Ser Tyr Ile Val Ser Gln Ile Ala Val Ala Tyr His Asn Ile Arg Asp 260 265 270

Ile Asp Lys Ala Leu Ser Ile Phe Asn Glu Leu Arg Lys Gln Asp Pro 275 280 285

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Ser Met Lys Ser Glu Leu Ser Tyr Leu Ala His Asn Leu Cys Glu Ile 305 310 315 320

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                            40
Gly Phe Gly Gly Tyr Val Cys Thr Thr Ser Gln Ser Ser Ala Leu Leu
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Ser His Leu Leu Val Thr His Pro Ile Leu Lys Ile Leu Thr Ala Ser
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90

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85

Ile Leu Cys Cys Asn Leu Ile Glu Asn Val Gln Arg Leu Gly Leu Thr

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- Ser Tyr Leu Lys Ser Asp Thr Cys Gly Cys Arg Ile Pro Val Asp Phe 130 135 140
- Ser Ser Thr Gln Ile Leu Leu Cys Leu Val Arg Ser Ile Leu Thr Ser 155 160
- Lys Pro Ala Cys Met Leu Thr Arg Lys Glu Thr Glu His Val Ser Ala 165 170 175
- Leu Ile Leu Arg Ala Phe Leu Leu Thr Ile Pro Glu Asn Ala Glu Gly 180 185 190
- His Ile Ile Leu Gly Lys Ser Leu Ile Val Pro Leu Lys Gly Gln Arg
- Val Ile Asp Ser Thr Val Leu Pro Gly Ile Leu Ile Glu Met Ser Glu 210 215 220
- Val Gln Leu Met Arg Leu Leu Pro Ile Lys Lys Ser Thr Ala Leu Lys 225 230 235 240
- Val Ala Leu Phe Cys Thr Thr Leu Ser Gly Asp Thr Ser Asp Thr Gly 245 250 255
- Glu Gly Thr Val Val Val Ser Tyr Gly Val Ser Leu Glu Asn Ala Val
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- Leu Asp Gln Leu Leu Asn Leu Gly Arg Gln Leu Ile Ser Asp His Val 275 280 285
- Asp Leu Val Leu Cys Gln Lys Val Ile His Pro Ser Leu Lys Gln Phe 290 295 300
- Leu Asn Met His Arg Ile Ile Ala Ile Asp Arg Ile Gly Val Thr Leu 305 310 315 320
- Met Glu Pro Leu Thr Lys Met Thr Gly Thr Gln Pro Ile Gly Ser Leu 325 330 335
- Gly Ser Ile Cys Pro Asn Ser Tyr Gly Ser Val Lys Asp Val Cys Thr 340 345 350
- Ala Lys Phe Gly Ser Gln His Phe Phe His Leu Ile Pro Asn Glu Ala 355 360 365
- Thr Ile Cys Ser Leu Leu Leu Cys Asn Arg Asn Asp Thr Ala Trp Asp 370 375 380
- Glu Leu Lys Leu Thr Cys Gln Thr Ala Leu His Val Leu Gln Leu Thr 385 390 395 400
- Leu Lys Glu Pro Trp Ala Leu Leu Gly Gly Gly Cys Thr Glu Thr His
 405 410 415

Leu Ala Ala Tyr Ile Arg His Lys Thr His Asn Asp Pro Glu Ser Ile 420 425 430

Leu Lys Asp Asp Glu Cys Thr Gln Thr Glu Leu Gln Leu Ile Ala Glu
435 440 445

Ala Phe Cys Ser Ala Leu Glu Ser Val Val Gly Ser Leu Glu His Asp 450 455 460

Gly Gly Glu Ile Leu Thr Asp Met Lys Tyr Gly His Leu Trp Ser Val 465 470 475 480

Gln Ala Asp Ser Pro Cys Val Ala Asn Trp Pro Asp Leu Leu Ser Gln
485 490 495

Cys Gly Cys Gly Leu Tyr Asn Ser Gln Glu Glu Leu Asn Trp Ser Phe 500 505 510

Leu Arg Ser Thr Arg Arg Pro Phe Val Pro Gln Ser Cys Leu Pro His 515 520 525

Glu Ala Val Gly Ser Ala Ser Asn Leu Thr Leu Asp Cys Leu Thr Ala 530 535 540

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<211> 1527

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Asp Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu Gly Met Lys 35 40 45

Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln Met Trp Gln 50 55 60

Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr Ala Asn Ile 65 70 75 80

Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln Val Arg Ser 85 90 95

Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn Phe Pro Gln 100 105 110

Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val Phe Thr Leu 115 120 125

Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr Ile Ile Arg 130 135 140

Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe Gly Tyr Trp 145 150 155 160

Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu Cys Asn Ala 165 170 175

Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr Gly Leu Phe 180 185 190

Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His Leu His Ala 195 200 205

Leu Phe Tyr Leu Phe Trp Arg Leu Val Gly Gly Leu Ser Thr Leu Arg 210 215 220

Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr Gln Arg Leu 225 230 235 240

Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe Leu Leu Tyr
245 250 255

Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu Asp Thr Leu

260 265 270

Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg Asp Ile Pro 275 280 285

Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu Asn Ala Thr 290 295 300

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<211> 988

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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Ala Ala Trp Ser Gly Ser Gly Arg Ser Leu Val Pro Ser Arg Ser Val
35 40 45

Ile Val Thr Arg Ser Gly Ala Ile Leu Pro Lys Pro Val Lys Met Ser 50 55 60

Phe Gly Leu Leu Arg Val Phe Ser Ile Val Ile Pro Phe Leu Tyr Val 65 70 75 80

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<211> 87

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<213> Homo sapiens

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Leu Met Cys Ile Pro Leu Cys Ala Phe Leu Tyr Asn His Ser Ser Phe 35 40 45

Asn Phe Pro Gly Glu Pro Ser Leu Ser Ala Ile Thr Thr Ser Phe Gln 50 55 60

Val Ser Ser Tyr Phe His His His Asn Gln Tyr Gly Ala Ile Ile Tyr

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80

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Leu Cys Thr Cys Ser Tyr Val

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<213> Homo sapiens

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<213> Homo sapiens

<400> 38

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Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr 35 40 45

Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln 50 55 60

Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr 65 70 75 80

Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro 85 90 95

Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr 100 105 110

Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser 115 120 125

Lys Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys 130 135 140

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                             40
Leu Pro Ser Gln Glu Leu Pro Gln Glu Asp Ser Leu Leu His Gly Gln
Phe Ser Gln Ala Val Thr Pro Leu Ala His His His Thr Asp Tyr Ser
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Lys Pro Thr Asp Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly
85 90 95

Ser Ser Asp His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala 100 105 110

Gln Leu Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe 115 120 125

Ser Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala 130 135 140

Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala Thr 145 150 155 160

Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr Pro Ser 165 170 175

Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro Val Thr Thr 180 185 190

Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr Val Phe Thr Arg

Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr Ala Val Leu Thr Thr 210 215 220

Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly Ser Leu Glu Thr Ile Pro 225 230 235 240

Phe Thr Glu Ile Ser Asn Leu Thr Leu Asn Thr Gly Asn Val Tyr Asn 245 250 255

Pro Thr Ala Leu Ser Met Ser Asn Val Glu Ser Ser Thr Met Asn Lys 260 265 270

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Gly Gln Cys Ser Arg Lys Ser Val Arg Pro Ser Ile 290 295 300

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<211> 1549

<212> DNA

<213> Homo sapiens

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Asp Lys Arg Val Asn Glu Trp Lys Thr Pro Gly Lys Lys Thr Ile Val 465 470 475 480

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Gln Pro Leu Ser Met Gln Ala Leu Pro Ala Gln Pro Glu Ser Leu Cys 565 570 575

Ile Val Glu Met Gly Gly Thr Glu Lys Gln Asp Glu Leu Gly Glu Arg 580 585 590

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Ile Val Ala Ile Ser Thr Asn Thr Leu Arg Ile Leu Ala Leu Glu Lys

690 695 700

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1020

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His Asp Phe Phe Gln His Val Glu Met His Leu Arg Ser Glu His Pro 1075 1080 1085

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Ile Asp Ile Gln Thr Arg Met Ala Gly Arg Ala Leu Glu Leu Leu Tyr 40

Leu Pro Glu Asn Lys Pro Cys Tyr Leu Leu Asp Ile Gly Cys Gly Thr 55

Gly Leu Ser Gly Ser Tyr Leu Ser Asp Glu Gly His Tyr Trp Val Gly

Leu Asp Ile Ser Pro Ala Met Leu Asp Glu Ala Val Asp Arg Glu Ile 90

Glu Gly Asp Leu Leu Gly Asp Met Gly Gln Gly Ile Pro Phe Lys

100 105 110

Pro Gly Thr Phe Asp Gly Cys Ile Ser Ile Ser Ala Val His Trp Leu 115 120 125

Cys Asn Ala Asn Lys Lys Ser Glu Asn Pro Ala Lys Arg Leu Tyr Cys 130 135 140

Phe Phe Ala Ser Leu Phe Ser Val Leu Val Arg Gly Ser Arg Ala Val 145 150 155 160

Leu Gln Leu Tyr Pro Glu Asn Ser Glu Gln Leu Glu Leu Ile Thr Thr 165 170 . 175

Gln Ala Thr Lys Ala Gly Phe Ser Gly Gly Met Val Val Asp Tyr Pro 180 185 190

Asn Ser Ala Lys Ala Lys Lys Phe Tyr Leu Cys Leu Phe Ser Gly Pro 195 200 205

Ser Thr Phe Ile Pro Glu Gly Leu Ser Glu Asn Gln Asp Glu Val Glu 210 215 220

Pro Arg Glu Ser Val Phe Thr Asn Glu Arg Phe Pro Leu Arg Met Ser 225 235 240

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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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Pro Thr Val Leu Arg Trp Ala Val Val Glu Ala Leu Leu Pro Ala Val 35 40 45

Cys Gly Thr Ser Pro Ala Leu Phe Phe Pro Val Pro Ile Gly Ser Leu 50 55 60

Arg Ala Arg Val Phe His Ser Lys Thr Val Leu Cys Asn Ser Phe Gln 65 70 75 80

Gln Ser Asn Asn Pro Pro Leu Gln Arg Ser Ser Ser Leu Ile Gln Leu 85 90 95

Thr Ser Gln Asn Ser Ser Pro Asn Gln Gln Arg Thr Pro Gln Val Ile
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Gly Val Met Gln Ser Gln Asn Ser Ser Gly Gly Asn Arg Gly Pro Gly
115 120 125

His Trp Ser Arg Ser Pro Val Thr Ser Val Ala Arg Lys Asp Thr Thr
130 135 140

Pro Thr Asp Ala Pro Lys Gly Thr Trp Pro Phe Ser Val Asp Ser Asp 145 150 155 160

Ser Ser Trp Ser Gln Leu Arg Ala Ala Arg Gly Pro Arg Cys Trp Glu 165 170 175

Cys Ala Phe Asn Cys Phe Met Arg Leu Leu Ala Arg Leu Trp Leu Glu 180 185 190

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<212> DNA

<213> Homo sapiens

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35 40 45

Lys Val Arg Arg Ser Thr Ser Arg Asp Arg Leu Asp Asp Ile Ile Val 50 55 60

Leu Thr Lys Asp Ile Gln Glu Gly Asp Thr Leu Asn Ala Ile Ala Leu 65 70 75 80

Gln Tyr Cys Cys Thr Val Ala Asp Ile Lys Arg Val Asn Asn Leu Ile 85 90. 95

Ser Asp Gln Asp Phe Phe Ala Leu Arg Ser Ile Lys Ile Pro Val Lys
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Lys Phe Ser Ser Leu Thr Glu Thr Leu Cys Pro Pro Lys Gly Arg Gln 115 120 125

Thr Ser Arg His Ser Ser Val Gln Tyr Ser Ser Glu Gln Gln Glu Ile 130 135 140

Leu Pro Ala Asn Asp Ser Leu Ala Tyr Ser Asp Ser Ala Gly Ser Phe 145 150 155 160

Leu Lys Glu Val Asp Arg Asp Ile Glu Gln Ile Val Lys Cys Thr Asp 165 170 175

Asn Lys Arg Glu Asn Leu His Glu Val Val Ser Ala Phe Thr Ala Gln 180 185 190

Gln Met Arg Phe Glu Pro Asp Asn Lys Asn Thr Gln Arg Lys Asp Pro 195 200 205

Tyr Tyr Gly Ala Asp Trp Gly Ile Gly Trp Trp Thr Ala Val Val Ile 210 215 220

Met Leu Ile Val Gly Ile Ile Thr Pro Val Phe Tyr Leu Leu Tyr Tyr

225 230 235 240

Glu Ile Leu Ala Lys Val Asp Val Ser His His Ser Thr Val Asp Ser 245 250 255

Ser His Leu His Ser Lys Ile Thr Pro Pro Ser Gln Gln Arg Glu Met 260 265 270

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Asp Lys Ala Lys Gly Arg Lys Glu Ser Glu Phe Asp Asp Glu Pro Lys
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Phe Met Ser Lys Val Ile Gly Ala Asn Lys Asn Gln Glu Glu Lys
Ser Gly Lys Trp Glu Gly Leu Val Tyr Ala Pro Pro Gly Lys Glu Lys
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Gln Arg Lys Thr Glu Glu Leu Glu Glu Glu Ser Phe Pro Glu Arg Ser
Lys Lys Glu Asp Arg Gly Lys Arg Ser Glu Gly Gly His Arg Gly Phe
Val Pro Glu Lys Asn Phe Arg Val Thr Ala Tyr Lys Ala Val Gln Glu
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Lys Ser Ser Ser Pro Pro Pro Arg Lys Thr Ser Glu Ser Arg Asp Lys
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Leu Gly Ala Lys Gly Asp Phe Pro Thr Gly Lys Ser Ser Phe Ser Ile
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Thr Arg Glu Ala Gln Val Asn Val Arg Met Asp Ser Phe Asp Glu Asp
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185

180

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195 200 205

- Asp Leu Val His Ser Asn Lys Lys Glu Gln Glu Phe Arg Ser Ile Phe 210 215 220
- Gln His Ile Gln Ser Ala Gln Ser Gln Arg Ser Pro Ser Glu Leu Phe 225 230 235 240
- Ala Gln His Ile Val Thr Ile Val His His Val Lys Glu His His Phe 245 250 255
- Gly Ser Ser Gly Met Thr Leu His Glu Arg Phe Thr Lys Tyr Leu Lys 260 265 270
- Arg Gly Thr Glu Glu Glu Ala Ala Lys Asn Lys Lys Ser Pro Glu Ile 275 280 285
- His Arg Arg Ile Asp Ile Ser Pro Ser Thr Phe Arg Lys His Gly Leu 290 295 300
- Ala His Asp Glu Met Lys Ser Pro Arg Glu Pro Gly Tyr Lys Ala Glu 305 310 315 320
- Gly Lys Tyr Lys Asp Asp Pro Val Asp Leu Arg Leu Asp Ile Glu Arg 325 330 335
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- Lys Thr Glu Lys Thr His Lys Gly Ser Lys Lys Gln Lys Lys His Pro 370 375 380
- Arg Ala Arg Asp Arg Ser Arg Ser Ser Ser Ser Ser Ser Gln Ser Ser 385 390 395 400
- His Ser Tyr Lys Ala Glu Glu Tyr Thr Glu Glu Thr Glu Glu Arg Glu 405 410 415
- Glu Ser Thr Thr Gly Phe Asp Lys Ser Arg Leu Gly Thr Lys Asp Phe
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- Val Gly Pro Ser Glu Arg Gly Gly Gly Arg Ala Arg Gly Thr Phe Gln
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Tyr Ser Asp Val Val Asp Glu Arg Ser Ile Val Lys Leu Cys Gly Tyr 50 55 60

Pro Leu Cys Gln Lys Lys Leu Gly Ile Val Pro Lys Gln Lys Tyr Lys
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Phe Cys Ser Asn Phe Cys Tyr Gln Ala Ser Lys Phe Phe Glu Ala Gln 100 105 110

Ile Pro Lys Thr Pro Val Trp Val Arg Glu Glu Glu Arg His Pro Asp 115 120 125

Phe Gln Leu Leu Lys Glu Glu Gln Ser Gly His Ser Gly Glu Glu Val 130 135 140

Gln Leu Cys Ser Lys Ala Ile Lys Thr Ser Asp Ile Asp Asn Pro Ser 145 150 155 160

His Phe Glu Lys Gln Tyr Glu Ser Ser Ser Ser Thr His Ser Asp 165 170 175

Ser Ser Ser Asp Asn Glu Gln Asp Phe Val Ser Ser Ile Leu Pro Gly 180 185 190

Asn Arg Pro Asn Ser Thr Asn Ile Arg Pro Gln Leu His Gln Lys Ser 195 200 205 Ile Met Lys Lys Lys Ala Gly His Lys Ala Asn Ser Lys His Lys His 210 215 220

- Lys Glu Gln Thr Val Val Asp Val Thr Glu Gln Leu Gly Asp Cys Lys 235 230 235 240
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- Tyr Ala Ser Val Cys Leu Lys Pro Glu Ala Ser Leu Val Lys Glu Glu 355 360 365
- Leu Asp Glu Asp Asp Ile Ile Ser Asp Pro Asp Ser Pro Phe Pro Ala 370 375 380
- Trp Arg Glu Ser Gln Asn Ser Leu Asp Glu Ser Leu Pro Phe Arg Gly 385 390 395 400
- Ser Gly Thr Ala Ile Lys Pro Leu Pro Ser Tyr Glu Asn Leu Lys Lys
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- Glu Thr Glu Lys Leu Asn Leu Arg Ile Arg Glu Phe Tyr Arg Gly Arg
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- Asp Ser Thr Phe Pro Leu Ile Asp Ser Ser Ser Gln Asn Gln Ile Arg 450 455 460
- Lys Arg Ile Val Leu Glu Lys Leu Ser Lys Val Leu Pro Gly Leu Leu 465 470 475
- Val Pro Leu Gln Ile Thr Leu Gly Asp Ile Tyr Thr Gln Leu Lys Asn 485 490 495
- Leu Val Arg Thr Phe Arg Leu Thr Asn Arg Asn Ile Ile His Lys Pro 500 500 510
- Ala Glu Trp Thr Leu Ile Ala Met Val Leu Leu Ser Leu Leu Thr Pro 515 520 525

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35 40 45

25

- Ser Leu Met Thr Ala Trp Ile Leu Leu Pro Val Ser Leu Ser Ala Phe 50 55 60
- Ser Ile Thr Gly Ile Trp Thr Val Tyr Ala Met Ala Val Met Asn His 65 70 75 80
- His Val Cys Pro Val Glu Asn Trp Ser Tyr Asn Glu Ser Cys Pro Pro 85 90 95
- Asp Pro Ala Glu Gln Gly Gly Pro Lys Thr Cys Cys Thr Leu Asp Asp
- Val Pro Leu Ile Ser Lys Cys Gly Ser Tyr Pro Pro Glu Ser Cys Leu 115 120 125
- Phe Ser Leu Ile Gly Asn Met Gly Ala Phe Met Val Ala Leu Ile Cys 130 135 140
- Leu Leu Arg Tyr Gly Gln Leu Leu Glu Gln Ser Arg His Ser Trp Val 145 150 155 160
- Asn Thr Thr Ala Leu Ile Thr Gly Cys Thr Asn Ala Ala Gly Leu Leu 165 170 175
- Val Val Gly Asn Phe Gln Val Asp His Ala Arg Ser Leu His Tyr Val
- Gly Ala Gly Val Ala Phe Pro Ala Gly Leu Leu Phe Val Cys Leu His
 195 200 205
- Cys Leu Ser Pro Thr Lys Gly Pro Pro Pro Arg Trp Thr Trp Leu Trp 210 215 220
- Pro Ile Cys Glu Val Cys Trp Leu Ser Ser Pro Leu Ser Pro Trp Ser 235 230 235 240
- Ser Val Glu Ser Ser Leu Ser Met Arg Val Leu Ser Cys Asn Met Gly 245 250 255
- Gln Pro Cys Val Ser Gly Cys Val Ser Ser Ile Ser Ser Phe Ser Met
 260 265 270
- Ala Pro Ser Ala Thr Ser Leu Gly Gln Ser Pro Gln Thr His Trp Trp 275 280 285
- Leu His Cys Ser Leu Pro Leu Ala Gly Pro Ala Ser Pro Pro Gly Ala 290 295 300
- Ala Ala Leu His Pro Pro Gln Leu Cys Pro Arg Glu His Arg Tyr Asp 315 320
- Leu Arg Ser Gly Glu Gly Gly Trp Pro Gly Ser Thr Ala Pro His Pro 325 330 335
- Ile Ser Ser Phe His Leu Phe Arg Thr Lys Asn Asn Phe Glu Lys Val

340 345 350

Phe Cys Trp Asp Leu Gly Phe Leu Thr Ser Gly Glu Val Ala Ile Pro

Cys Pro Pro Val Pro Trp Arg Ser Gly Pro Cys Gln Leu Pro Gln Leu 370 375 380

His Asp Leu Leu Pro Thr Pro Arg Cys Arg Phe Val Phe Lys Gly His 385 390 395 400

Leu Ser Ser Leu Thr Gln Pro Ala Leu Gln Val Pro Ser Thr Pro Ser 405 410 415

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<212> PRT

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Ser Arg Arg Ser Leu Thr Asn Ser His Leu Glu Lys Lys Lys Cys Asp 50 55 60

Glu Tyr Ile Pro Gly Thr Thr Ser Leu Gly Met Phe Val Phe Asn Leu 65 70 75 80

Ser Asn Ser Met Met Gly Ser Gly Ile Trp Asp Ser Leu Cys Pro Gly 85 90 95

Asn Thr Gly Ile Leu Leu Phe Leu Val Leu Leu Thr Ser Val Thr Leu 100 105 110

Leu Ser Ile Tyr Ser Ile Asn Leu Leu Leu Ile Cys Ser Lys Glu Thr 115 120 125

Gly Cys Met Val Tyr Glu Lys Leu Gly Glu Gln Val Phe Gly Thr Thr 130 135 140

Gly Lys Phe Val Ile Phe Gly Ala Thr Ser Leu Gln Asn Thr Gly Ala 145 150 155 160

Met Leu Ser Tyr Leu Phe Ile Val Lys Asn Glu Leu Pro Ser Ala Ile 165 170 175

Lys Phe Leu Met Gly Lys Glu Glu Thr Phe Ser Ala Trp Tyr Val Asp 180 185 190

Gly Arg Val Leu Val Val Ile Val Thr Phe Gly Ile Ile Leu Pro Leu 195 200 205

Cys Leu Leu Lys Asn Leu Gly Tyr Leu Gly Tyr Thr Ser Gly Phe Ser 210 215 220

Leu Ser Cys Met Val Phe Phe Leu Ile Val Val Ile Tyr Lys Lys Phe

225 230 235 240

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Ser Thr Asn Ala Asp Thr Cys Thr Pro Lys Tyr Val Thr Phe Asn Ser 260 265 270

Lys Thr Val Tyr Ala Leu Pro Thr Ile Ala Cys Ala Phe Val Cys His 275 280 285

Pro Ser Val Leu Pro Ile Tyr Ser Glu Leu Lys Asp Arg Ser Gln Lys 290 295 300

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Thr Lys Phe Asn Leu Cys Arg His Thr Val Val Thr Cys Ile Leu Leu 385 390 395 400

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Pro Ser Ser Leu Tyr Leu Lys Ile Thr Asp Gln Asp Gly Asp Lys Gly 435 440 445

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<211> 1999

<212> DNA

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Gln His Phe Leu Asp Gly Tyr Leu Leu Gly Pro Phe Ile Arg Lys Arg

Glu Arg Met Gly Trp Phe Cys Met Gly Ser Cys Leu Gly Val Lys Ile 70 75

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Ile Pro Ile Leu Gly Leu Val Leu Arg Thr Leu Tyr Met Cys Leu Phe 105

Thr Ser Gly Leu Pro Ala Ile Ala Phe Leu Pro Phe Pro Ile Leu 120

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25

20

35

40

Leu Gly His Pro Leu Phe Pro Ser Ser Ser Ala Pro Thr Gln Val Thr
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45

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Pro Pro Asp Ala Val Leu Met Ser Ile Phe Gln Glu Arg Asp Gly Leu
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- Asn Cys Leu Gly Ile Ser Val Leu Ala Glu Cys Leu Asp Cys Pro Glu
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- Ser Pro Glu Asp Arg Glu Glu Leu Val Asp Gly Pro Arg Pro Arg 235 240
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- Cys Pro Phe Glu Lys Pro Arg Asp Ala Ala Cys Val Phe Trp Asp Asn 275 280 285
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- Pro Thr Pro Arg Asp Ser Leu Ala Ala Cys Ala Ala Glu Gly Lys Ile 325 330 335

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Glu Cys Tyr Asp Thr Arg Thr Glu Ser Trp His Thr Lys Pro Ser Met 355 360 365

Leu Thr Gln Arg Cys Ser His Gly Met Val Glu Ala Asn Gly Leu Ile 370 375 380

Tyr Val Cys Gly Gly Ser Leu Gly Asn Asn Val Ser Gly Arg Val Leu 385 390 395 400

Asn Ser Cys Glu Val Tyr Asp Pro Ala Thr Glu Thr Trp Thr Glu Leu 405 410 415

Cys Pro Met Ile Glu Ala Arg Lys Asn His Gly Leu Val Phe Val Lys 420 425 430

Asp Lys Ile Phe Ala Val Gly Gly Gln Asn Gly Leu Gly Gly Leu Asp 435 440 445

Asn Val Glu Tyr Tyr Asp Ile Lys Leu Asn Glu Trp Lys Met Val Ser 450 460

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Lys Ile Thr Gly Lys Ala Met Leu Leu Glu Ile Phe Trp Ser Gly Ser
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Thr Ile Tyr Ser His Lys Glu Lys Phe Lys Ser Asn Asp Thr Phe Leu

115

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- Arg Thr Leu Leu Met Leu Asn Gly Thr Lys Gln Lys Gln Val Glu Gly 210 215 220
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Gly Leu Thr His Leu Asn Glu Leu Leu Met Ala Cys Lys Ser His Lys Glu Thr Thr Ser Val His Thr Asp Trp Leu Leu Asp Leu Tyr Ala Gly. 470 Asn Ile Lys Thr Leu Gln Lys Leu Pro His Ile Leu Lys Glu Leu Pro 485 490 Glu Asn Leu Lys Val Cys Pro Gly Val His Thr Glu Ala Leu Met Ile 500 505 Thr Leu Glu Met Met Cys Arg Ser Val Met Glu Phe Ser . <210> 81 <211> 2625 <212> DNA <213> Homo sapiens <220> <221> unsure <222> (2559) <220> <221> unsure <222> (2561) <400> 81 gtetectage accgeatetg tecaggaage caetgeetge ttgttgetea tetgtagttt 60 geaggtgggg gttgetttte etttgttetg ceaggegget teagggetee etgtetgtag 120 gtcagtatat ttcaccagtt ctgaaaaccc caacctactc cttgacagcc attgtttcct 180 ctgeetetgg gacatecate aaatgtaegt tageeeteat tecatettee gegteeetta 240 ttetgtcete tgeetteeca egttattete tgtaataatt tatetgaaat ttttttatet 300 tectatteae tgggtaagtt ettaatette etatttaetg tttetetett etactgtate 360 tagactggca ccaaatatgt ccactgagta cattagtgtt tcatttctaa aagagctgtt 420 tggttttctt tcaaatttgc tgtatctgtt tttagaattt tcagttcccg tcatattcag 480 agtttgttgt tcatttctgc aaacgctgag cgtagctgcc tcacggtgcg tctgcggtgc 540 catctgagtg ttcttggcag cactgccagg tctccctggg agctgcgctc tttgaccctg 600 tgacgtcctg aggcctgggc cagatgctgc ttcctccagg gaagatttgt tctccctccc 660 agtagetece cagggacete ceacaceaet geeetgggee etgtgtgtat aggeeeagat 720 ttttctctgt gtcctttatt accagctctg tttacagatc cctggagtca ggggaagggg 780 tgagetcaga tetgaggeca agaggecatt teccagetgg etgeagetga geetggtgge 840 tgtgtctgag cgtcgtggag ccagggtcca cggcacccag gtggcggggg gcaggcgccc 900 tgaccageca eggecteaaa gtgactetee tgetetgete eagecacace tgeatgetgt 960 ggcgggcgct ggcggtggag cctcgcctag ctgcccaggt cctggggctg ctgctggaga 1020 agatgagtag ggacgtecet tteaaggaga geegggeett eetgetggge egeaceeeag 1080 accgcgtggc cacgctgctg cctctctcgg ctacctgtgc actgtttgag gtcatgtcca 1140 egectgeage ggggecegeg gtgetegage tetacececa getgtttgtg gtgettetge 1200 tgcgcgtcag ctgcaccgtg ggtgtccagc tgccccggaa cctgcaggcc caggaaagga 1260 ggggtgccag tccagcccta gccaccagga acctggaaec ctgcagctct gcagtggaca 1320 ccctgcggtc catgctactc cgcagcggca gcgaggatgt ggtacagcgc atggacctgg 1380 agggaggetg ggaactgete aggacetegg eggggeatga ggagggggee accaggttgg 1440 ccagggccat ggctgagcac gcagggcccc gactececct ggtgctgaag acgctggcat 1500 gcacacacag cagtgcgtat gagaaccaga gggtgaccac caccgccttc ctggccgagc 1560 tgctgaacag caacgtggcc aacgacetca tgctettgga etegetgetg gagageetgg 1620 cggctcgcca gaaggacaca tgcgccagcg tgcggaggct ggtgctccgc ggcctggcca 1680 acctggcete eggetgeeet gacaaggtge gaacecaegg ecceeagete etcacageca 1740 tgattggcgg gctggacgac ggggacaacc ctcacagccc agtggccctg gaggccatgc 1800

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Gly Trp Glu Leu Leu Arg Thr Ser Ala Gly His Glu Glu Gly Ala Thr
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Val Leu Lys Thr Leu Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln
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205

Arg Val Thr Thr Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val

195

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- Leu Ala Asn Leu Ala Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly 245 250 255
- Pro Gln Leu Leu Thr Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn 260 265 270
- Pro His Ser Pro Val Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu 275 280 285
- Val His Leu Val Glu Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val 290 295 300
- Ala Ile Arg Ile Arg Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg 305 310 315 320
- Thr Ala Ser Ile Arg Leu Phe Gly His Leu Asn Lys Val Cys His Gly 325 330 335
- Asp Cys Glu Asp Val Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro 340 345 350
- Leu Leu His Leu Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys 355 360 365
- Arg Phe Ala Leu Arg Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu 370 375 380
- Ser Ala Ala Phe Gln Lys His Leu Gln Glu Gly Arg Ala Leu His Phe 385 390 395 400
- Gly Glu Phe Leu Asn Thr Thr Cys Lys His Leu Met His His Phe Pro 405 410 415
- Asp Leu Leu Gly Arg Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser 420 425 430
- Ser Trp Glu Asn Val Arg Ala Ala Ala Pro Leu Phe Thr Gly Lys His 435 440 445
- His Pro Leu Pro His Pro His Ala Ala Arg Gln Pro Arg Leu Met Pro 450 455 460
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Arg Ser Ile Thr Ala Pro Leu Ala Ala His Ile Ser Leu Val Asn Lys
Ala Ala Val Asp Tyr Phe Phe Val Glu Leu His Leu Glu Ala His Tyr
Glu Ala Leu Arg His Phe Leu Leu Met Glu Asp Gly Glu Phe Ala Gln
Ser Leu Ser Asp Leu Leu Phe Glu Lys Leu Gly Ala Gly Gln Thr Pro
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Arg Arg Ala Ala Gln Pro Ala Gly Ala Glu Leu Cys Ala Asp Lys Ala
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140

135

130

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Ile Val Ile Thr Glu Gly Cys Leu Ser Lys Tyr Ser Gly Val Phe Ser 180 185 190

Phe Leu Gln Leu Lys Leu Met Met Trp Ala Leu Lys Asp Val Cys 195 200 205

Phe His Leu Lys Arg Thr Ala Leu Leu Ser His Met Ala Gly Ser Val 210 215 220

Gln Phe Arg Gln Leu Gln Leu Phe Lys His Glu Met Gln His Phe Val 225 230 235 240

Lys Val Ile Gln Gly Tyr Ile Ala Asn Gln Ile Leu His Val Thr Trp
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Cys Glu Phe Arg Ala Arg Leu Ala Thr Val Gly Asp Leu Glu Glu Ile 260 265 270

Gln Arg Ala His Ala Glu Tyr Leu His Lys Ala Val Phe Arg Gly Leu 275 280 285

Leu Thr Glu Lys Ala Ala Pro Val Met Asn Val Ile His Ser Ile Phe 290 295 300

Ser Leu Val Leu Lys Phe Arg Ser Gln Leu Ile Ser Gln Ala Trp Gly 305 310 315 320

Pro Pro Gly Gly Pro Arg Gly Ala Glu His Pro Asn Phe Ala Leu Met 325 330 335

Gln Gln Ser Tyr Asn Thr Phe Lys Tyr Tyr Ser His Phe Leu Phe Lys 340 345 350

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Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu
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Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu
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Lys Arg Tyr Ala His Ala Leu Val Phe Gly Ile Leu Leu Thr Cys Arg
Leu Leu Ile Ala Arg Lys Pro Glu Asp Arg Ser Ser Glu Lys Lys Pro
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Gln Gly Lys Val Lys Val Ser 165

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Met Leu Pro His Cys Pro Leu Gln Ser Leu Ser Gly Ser Leu Val Leu 50 55 60

Asp Cys Cys Ser Gly Lys Leu Tyr Arg Ala Leu Leu Ser Gln Ser Ser 65 70 75 80

Leu Leu Gln Leu Gln Asn Thr Cys Leu Asp Cys Glu Lys Met Ala 85 90 95

Ala Leu His Cys Ala Leu Tyr Cys Gly Gln Gly Ala Gln Phe Leu Glu 100 105 110

Ala Gln Ile Ile Gln Trp Ile Ser Glu Asn Val Ser Ala Cys His Ser 115 120 125

Phe Asp Leu Ile Gln Glu Phe Ile Ile Ala Ser Ser Tyr Trp Ser Val 130 135 140

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Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn 35 40 45

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Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu Glu Val Gly Cys Gly 65 70 75 80

Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
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Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu Ile Lys Ser Ile Ala
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Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu 115 120 125

Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Cys Thr 130 135 140

Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val 145 150 155 160

Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr Phe Met Glu His Val 165 170 175

Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp Gln Gln Val Leu Asp 180 185 190

Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn Leu Thr Arg Glu Ser 195 200 205

Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys Leu Lys Leu Gln His 210 215 220

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Glu Ala Met Asp Asp Val Val Glu Gln Asp Ala Glu Glu Glu Ala 235

Glu Glu Gly Pro Pro Leu Gly Ala Ile Pro Ile Thr Asp Cys Leu Phe

Cys Ser His His Ser Ser Ser Leu Met Lys Asn Val Ala His Met Thr 265

Lys Asp His Ser Phe Phe Ile Pro Asp Ile Glu Tyr Leu Ser Asp Ile

Lys Gly Leu Ile Lys Tyr Leu Gly Glu Lys Val Gly Val Gly Lys Ile

Cys Leu Trp Cys Asn Glu Lys Gly Lys Ser Phe Tyr Ser Thr Glu Ala

Val Gln Ala His Met Asn Asp Lys Ser His Cys Lys Leu Phe Thr Asp

Gly Asp Ala Ala Leu Glu Phe Ala Asp Phe Tyr Asp Phe Arg Ser Ser 345

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Leu Pro Ser Gly Ala Arg Val Gly His Arg Ser Leu Met Arg Tyr Tyr

Lys Gln Arg Phe Gly Leu Ser Arg Ala Val Ala Lys Asn Arg

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35

40

Lys Thr Ser Pro Met Arg Met Leu Tyr Met Thr Ser Leu Met Ala Pro 50 55 60

45

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Glu Asp Val Val Tyr Asp Ile Ala Asn Glu Asp Ala Leu Gln Asp Ile 100 105 110

Ala Asn Glu Val Ala Val Tyr Asp Ile Ala Asn Glu Asp Ile Val Tyr 115 120 125

Asp Ile Ala Asn Glu Asp Ala Leu Tyr Asp Ile Thr Asn Glu Asp Ala 130 135 140

Val Tyr Asn Ile Ala Asn Glu Asp Ala Val Tyr Gly Ile Ala Asn Glu 145 150 155 160

Asp Ala Val Tyr Glu Phe Ala Asn Lys Asp Ala Val Tyr Asp Ile Ala 165 170 175

Asn Glu Asp Thr Val Gln Asp Ile Cys Lys Lys Glu Asp Ala Ala Asn 180 185 190

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Leu Arg Lys Lys Arg His Leu 210 215

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<212> DNA

<213> Homo sapiens

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Cys Pro Cys Glu Tyr Leu Arg Lys Val Ser Glu Cys Arg Gln Met Gly
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Gly Ser Ser Gly Val Gly Val Gly Arg Gly Pro Cys Pro Pro Cys Leu
Asp Phe Ala Pro Leu Gly Pro Ala Gly Ser Arg Pro Val Asn Val Ser
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Ser Ser Gly Thr Asp Ser Val Cys Ser Trp Pro Trp Val His Leu Thr
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Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn
Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu
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Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr
Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu
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Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp
                                105
Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile
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Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu
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                        135
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser
Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser
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Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val
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Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg 275 280

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<400> 111

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<210> 112

<211> 487

<212> PRT

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<400> 112

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- Phe Thr Ala Asp Gly Asp Gln Val Phe Ala Gly Arg Tyr Tyr Ser Ser 35 40 45
- Glu Asn Thr Arg Pro Lys Phe Leu Ser Arg Asp Val Asp Ser Glu Ile 50 55 60
- Ser Asp Leu Glu Asn Glu Val Glu Asn Lys Thr Ala Gln Ile Leu Asn 65 70 75 80
- Leu Gln Gln His Leu Ser Ala Leu Glu Lys Asp Ile Lys His Asn Glu 85 90 95
- Glu Leu Leu Lys Arg Cys Gln Leu His Tyr Lys Glu Leu Lys Met Lys 100 105 110
- Ile Arg Lys Asn Ile Ser Glu Ile Arg Glu Leu Glu Asn Ile Glu Glu
 115 120 125
- His Gln Ser Val Asp Ile Ala Thr Leu Glu Asp Glu Ala Gln Glu Asn 130 135 140
- Lys Ser Lys Met Lys Met Val Glu Glu His Met Glu Gln Gln Lys Glu 145 150 155 160
- Asn Met Glu His Leu Lys Ser Leu Lys Ile Glu Ala Glu Asn Lys Tyr 165 170 175
- Asp Ala Ile Lys Phe Lys Ile Asn Gln Leu Ser Glu Leu Ala Asp Pro 180 185 190
- Leu Lys Asp Glu Leu Asn Leu Ala Asp Ser Glu Val Asp Asn Gln Lys
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- Arg Gly Lys Arg His Tyr Glu Glu Lys Gln Lys Glu His Leu Asp Thr 210 215 220
- Leu Asn Lys Lys Lys Arg Glu Leu Asp Met Lys Glu Lys Glu Leu Glu 225 230 230 235
- Glu Lys Met Ser Gln Ala Arg Gln Ile Cys Pro Glu Arg Ile Glu Val 245 250 255
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<210> 114

<211> 207

<212> PRT

<213> Homo sapiens

<400> 114

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Leu Gly Ile Phe Gly Thr Val Gln Tyr Arg Ser Arg Tyr Leu Ile Leu 50 55 60

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Ala Arg Thr Gly Lys Val Leu Gly Leu Ser Pro Ser Pro Arg Thr Pro
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Trp Trp Trp Arg Ile His Pro Ala Val Ala Ala Val Phe Arg
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118

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- Glu Ala Ser Ser Thr Arg Ile Cys Leu Lys Glu Leu Gly Thr Phe Ala 130 135 140
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Thr Glu Glu Gly Arg Gln Ala Leu Glu Pro Leu Pro Gln Gly Ile Gln 720

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Ser Lys Val Gln Glu Ser Thr Lys Gly Pro Asp Glu Ala Lys Ile Lys 115 120 125

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Lys Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu

Asp Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala 85

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Glu Leu Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Lys 115 120 125

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Phe Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu 145 150 155 160

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Ile Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile 195 200 205

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gguerectaa acayeayeta ayetacaaaa aqeaaacaaa accacacata thoobacana acay
ctgcattcca ccacatatcc accettgaga agtatgtcaa aagactgcag actatagatt 4980
- 3-3 3-4-9-0-44 adjactycag actatagatt 4980

tttttttaat ataggattat aaatcageta gtgaaagace tcagagcagt tgtaagtaga 5040 tctgccatct agaactcata ttctaaaggg aagtgattte tcagaacagt gatgttctgg 5100 aatatgtatt atttattta acacttttt aataaaatct ttattataaa ccatgaaaaa 5160 aaaaaaaaaa

<210> 132

<211> 695

<212> PRT

<213> Homo sapiens

<400> 132

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Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly 115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Arg Cys 180 185 190

Pro Met Arg Ser Leu Gly Ala Asn Pro Trp Tyr Cys Gly Asp Pro Ala 195 200 205

Arg Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys Glu 210 215 220

Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val Cys 235 240

Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr Glu 245 250 255

Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro Ala

270

Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr Pro 280 285

265

- Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala Pro 295
- Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg Pro 310 315
- Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala Asn 330
- Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly Ser 345
- Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala Asp
- Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp Asn
- Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn Leu 395
- Ile Leu Leu Asp Leu Gly Asn Asn Ile Ala Thr Val Glu Asn Asn 405 410
- Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser Asn 425
- Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn Leu 440 445
- Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro Gly 455
- Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn Asn
- Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu Ser
- Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala Gly
- Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly Asn 520
- Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala Glu 535
- Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr Pro
- Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu Ile 565 570
- Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His Ser

580 585

590

PCT/US99/18298

Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser Tyr 595 600 605

Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu Leu 610 620

Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val Phe 625 630 635 640

Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser Ser 645 650 655

Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr Trp 660 665 670

His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp Cys 675 680 685

Gly Ser His Ser Leu Ser Asp 690 695

<210> 133

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 133

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<210> 134

<211> 109

<212> PRT <213> Homo sapiens

<400> 134

Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser Val
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Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu Asp Leu 20 25 30

Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly Thr Arg Thr 35 40 45

Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly Thr Ala Ser Pro 50 55 60

Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro Thr Val Ser Arg Leu 65 70 75 80

Glu Ala Leu Thr Arg Ala Val Gln Val Ala Glu Pro Leu Gly Ser Cys
85 90 95

Gly Phe Gln Gly Gly Pro Cys Pro Gly Arg Arg Arg Asp 100 105

<210> 135

<211> 839

<212> DNA

<213> Homo sapiens

<400> 135

<210> 136

<211> 250

<212> PRT

<213> Homo sapiens

<400> 136

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Leu Lys Ser Ser Arg Ser Leu Ile Thr Pro Gln Val Pro Ala Cys Thr

Gly Phe Phe Leu Ser Leu Leu Pro Lys Ser Thr Pro Asn Val Thr Ser

35

40

45

Phe His Gln Tyr Arg Leu Leu His Thr Thr Leu Ser Arg Lys Gly Leu 55

Glu Glu Phe Phe Asp Asp Pro Lys Asn Trp Gly Gln Glu Lys Val Lys

Ser Gly Ala Ala Trp Thr Cys Gln Gln Leu Arg Asn Lys Ser Asn Glu

Asp Leu His Lys Leu Trp Tyr Val Leu Leu Lys Glu Arg Asn Met Leu 105

Leu Thr Leu Glu Gln Glu Ala Lys Arg Gln Arg Leu Pro Met Pro Ser 120

Pro Glu Arg Leu Asp Lys Val Val Asp Ser Met Asp Ala Leu Asp Lys 140

Val Val Gln Glu Arg Glu Asp Ala Leu Arg Leu Leu Gln Thr Gly Gln 155

Glu Arg Ala Arg Pro Gly Ala Trp Arg Arg Asp Ile Phe Gly Arg Ile 165 170

Ile Trp His Lys Phe Lys Gln Trp Val Ile Pro Trp His Leu Asn Lys

Arg Tyr Asn Arg Lys Arg Phe Phe Ala Leu Pro Tyr Val Asp His Phe

Leu Arg Leu Glu Arg Glu Lys Arg Ala Arg Ile Lys Ala Arg Lys Glu 210 220

Asn Leu Glu Arg Lys Lys Ala Lys Ile Leu Leu Lys Lys Phe Pro His 230 235

Leu Ala Glu Ala Gln Lys Ser Ser Leu Val 245

<210> 137

<211> 1067

<212> DNA

<213> Homo sapiens

<400> 137

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ccatggagca gcaaccctga gtccctaaag gcagcagctc aaggatggca ctcagatctc 780 catggcccag caaggccaag ataaatctac caccccaggc acctgtgagc caacaggtta 840 attagtccat taattttagt gggacctgca tatgttgaaa attaccaata ctgactgaca 900 tgtgatgctg acctatgata aggttgagta tttattagat gggaagggaa atttggggat 960 tatttateet eetggggaca gtttggggag gattatttat tgtatttata ttgaattatg 1020 tactttttc aataaagtct tatttttgtg gcaaaaaaaa aaaaaaa <210> 138 <211> 189 <212> PRT <213> Homo sapiens <400> 138 Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln 25 Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His 40 45 Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu 105 Pro Ser Leu Leu Pro Asp Ser Pro Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu 150 155 Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala 170 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro 180

<210> 139

<211> 1785

<212> DNA

<213> Homo sapiens

<400> 139

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acattectga tggttgtagg aatcagtaga ccctgtatgg aaagcaatag gataatattt 300
  cataggatca aattaaaatg ttcacagcat tggttccagg aaattggctt ctggagaatt 360
  tatactccag aaacaattca acaaaagaac acagctctgt gcatgcagat gctcattagc 420
  ccatcaccta gagtaaggga aagtggagat cccaatgaac aacaatgaga tgggttagcg 480
  aactgtgacc tatcagccca atggacattt aagcaatcac tgaaaagtag aaacatgaag 540
  atattacaca acatggaaac tgtttatgga gtatatttag gtaaaaagga aaaaaaggca 600
  gaactgtata tetgtggttg gatatacttt tttttttaa tattaagcac caaccaaaag 660
  aagaaaggag gatagaaaaa ataaaatgga agatgtaggg tgggcagatt agggctgcgt 720
  ttgttgcttg ctttcatgtt accatcatag cgtttttgcc acttacaaag gaggaaaaaa 780
  atcaattctg tgccaaccca gacaacagag acctgagtgg gggttgggaa gagagatttt 840
  tragcaraga atragacter tteteraaag agetgtgtgg cettracetg caaggegace 900
  tettecacaa geagaggeea ggacaaaaag aggeacetgt gagegacaaa gaeggtttee 960
  ttggttteec teaeggegee aageggagtg geegeeteec accaeaggge eccetaatgg 1020
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 <211> 86
 <212> PRT
 <213> Homo sapiens
 <400> 140
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Gly Ala Lys Gly Lys Cys Ile Ser Arg Thr Gly Gly Phe Ile Ile Pro
Ser Val Ser Asp Arg Met Val Thr Glu Ala Leu Trp Thr Tyr Phe Pro
Ala Phe Ser Ser His Gln Gly Trp Val Cys Thr Gly Gly Lys Gly Pro
Gln Glu Glu Ala Leu Ile Phe Asn Lys Thr Cys Phe Leu Arg Thr Ala
 65
                     70
Asn Lys Arg Lys Ala Gln
<210> 141
<211> 947
<212> DNA
<213> Homo sapiens
<400> 141
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tagettteec tetteeggea teetggaaag tggatacetg tggeetteet tteaetttga 120

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aagettacae eeteattttg aetacaaeta ataetaaaag ettggeatet tgettgagat 180
  tagtgtttgc tatgccaaac accttctcct ctttctattg aaagcaaaac ataggaaaat 240
  aatttgaaat acttttaagg catcttaaaa acatgacttt ttcatcttat ggaaaagcag 300
  accaattttg ctttttttc ccaacttgtt ctccagactg tgccaataaa atgtgttcat 360
  agcaggaaaa tttggaaaat acagaaaagc actatgaaga aaacaaaatg tacccaaaat 420
  cccatcactc agataacatc actgttaatg ttttgatatg tatttccagt cttttctatt 480
  gtgttaattt ttcattttgt ttttgaataa ataactttca ggaaagaaat tgagcctttt 540
 ctgccacctc tgaagcctga ttactgtgtg aagcaggcca tgaaggccat cctcactgac 600
  cageceatga tetgeaetee eegeeteatg tacategtga eetteatgaa gageateeta 660
  ccatttgaag cagttgtgtg catgtatcgg ttcctaggag cggacaagtg tatgtacccc 720
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 <210> 142
 <211> 65
 <212> PRT
 <213> Homo sapiens
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 Met Tyr Ile Val Thr Phe Met Lys Ser Ile Leu Pro Phe Glu Ala Val
                                  25
 Val Cys Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys Met Tyr Pro Phe
 Ile Ala Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu Ala Lys Asn Gly
                         55
 Ile
  65
 <210> 143
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 <212> DNA
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geoegegeee egageeegee geogecette gagggegeee caggeegege catggtgaag 180
gtgacgttca actccgctct ggcccagaag gaggccaaga aggacgagcc caagagcggc 240
gaggaggege teateateee eecegaegee gtegeggtgg actgeaagga eecagatgat 300
gtggtaccag ttggccaaag aagagcctgg tgttggtgca tgtgctttgg actagcattt 360
atgettgeag gtgttattet aggaggagea taettgtaca aatattttge aetteaacea 420
gatgacgtgt actactgtgg aataaagtac atcaaagatg atgtcatctt aaatgagccc 480
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aacattgttc atgactttaa caagaaactt acagcctatt tagatcttaa cctggataag 660
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atttgttett gaacagteaa gaaaaacatt attgaggaaa attaatatca cagcataace 1020
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<210> 144

<211> 266

<212> PRT

<213> Homo sapiens

<400> 144

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Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp
20 25 30

Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly
35 40 45

Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met 50 55 60

Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala 65 70 75 80

Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp 85 90 95

Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr 100 105 110

Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu 115 120 125

Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn 130 135 140

Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn 145 150 155 160

Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro 165 170 175

Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly Thr Tyr 180 185 190

Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg
195 200 205

Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His 210 215 220

Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile
225 230 235 240

Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn 245 250 255

Lys Phe Ala Val Glu Thr Leu Ile Cys Ser 260 265

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 caactgacct geoctattee tggctgatet catgetgetg aagtteaagg egetggacae 180
 actaccctga tttttgttgc acctggccta gcctcattaa cttggcaatt agttggtggt 240
 tcatctttct tttttaagta gttgttccat gctgttgttt tttgttttat ctttcattgc 360
 ctttccctct gcagtcaaca ttatgacctg gggactccag catccttcaa gcaagccatt 420
 teegaagaag gtgaaaagaa geeaggatga ttggcacete eteeteetee teetettett 480
 cetetteeet tgeecageee ceteetgtge gtgtgtttea gacaacacag gagecageae 540
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 cagtttgtgc aataagaaga ttttttttt ctttttaaat cttcattata ttttctttga 660
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 acaaacaaac tgatggaaaa aaagagttaa ctattttatt tatttcaata tttaaaagga 780
 aaaaagtgct gacatggcac agtatttttg tttaaagtac ctcctacttc aaaagttaag 840
 cgcaattttg tgaagacatg aaatcataag agtacttaat gtaaaataaa agactgcata 900
 ttaactctaa agaaaaatge eccacatttt aaataagaaa ataaagatca actetgetet 960
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 <213> Homo sapiens
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Asn Ile Met Thr Trp Gly Leu Gln His Pro Ser Ser Lys Pro Phe Pro
                                25
Lys Lys Val Lys Arg Ser Gln Asp Asp Trp His Leu Leu Leu Leu Leu
Leu Phe Phe Leu Phe Pro Cys Pro Ala Pro Ser Cys Ala Cys Val Ser
                        55
Asp Asn Thr Gly Ala Ser Thr Gly Val Glu Asn Pro Ala Ala Gln Leu
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<212> PRT

<213> Homo sapiens

<400> 148

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- Pro Ala Ser Gly Pro Gly Ala Val Val Arg Pro Pro Lys Ala Pro Glu 50 55 60
- Asp Phe Ser Gln Asn Trp Lys Ala Leu Gln Glu Trp Leu Leu Lys Gln 65 70 75 80
- Lys Ser Gln Ala Pro Glu Lys Pro Leu Val Ile Ser Gln Met Gly Ser
- Lys Lys Lys Pro Lys Ile Ile Gln Gln Asn Lys Lys Glu Thr Ser Pro
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- Pro Arg Thr Lys Ala Ser Gly Thr Glu His Asn Lys Lys Gly Thr Lys 145 150 155 160
- Glu Arg Thr Asn Gly Asp Ile Val Pro Glu Arg Gly Asp Ile Glu His
- Lys Lys Arg Lys Ala Lys Glu Ala Ala Pro Ala Pro Pro Thr Glu Glu
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- Asp Ile Trp Phe Asp Asp Val Asp Pro Ala Asp Ile Glu Ala Ala Ile 195 200 205
- Gly Pro Glu Ala Ala Lys Ile Ala Arg Lys Gln Leu Gly Gln Ser Glu 210 215 220
- Gly Ser Val Ser Leu Ser Leu Val Lys Glu Gln Ala Phe Gly Gly Leu 225 230 235 240
- Thr Arg Ala Leu Ala Leu Asp Cys Glu Met Val Gly Val Gly Pro Lys 245 250 255
- Gly Glu Glu Ser Met Ala Ala Arg Val Ser Ile Val Asn Gln Tyr Gly
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- Lys Cys Val Tyr Asp Lys Tyr Val Lys Pro Thr Glu Pro Val Thr Asp
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- Tyr Arg Thr Ala Val Ser Gly Ile Arg Pro Glu Asn Leu Lys Gln Gly 290 295 300

Glu Glu Leu Glu Val Val Gln Lys Glu Val Ala Glu Met Leu Lys Gly 315 320

Arg Ile Leu Val Gly His Ala Leu His Asn Asp Leu Lys Val Leu Phe 325 330 335

Leu Asp His Pro Lys Lys Lys Ile Arg Asp Thr Gln Lys Tyr Lys Pro 340 345 350

Phe Lys Ser Gln Val Lys Ser Gly Arg Pro Ser Leu Arg Leu Leu Ser 355 360 365

Glu Lys Ile Leu Gly Leu Gln Val Gln Gln Ala Glu His Cys Ser Ile 370 375 380

Gln Asp Ala Gln Ala Ala Met Arg Leu Tyr Val Met Val Lys Lys Glu 385 390 395 400

Trp Glu Ser Met Ala Arg Asp Arg Arg Pro Leu Leu Thr Ala Pro Asp
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His Cys Ser Asp Asp Ala 420

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<213> Homo sapiens

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<211> 406

<212> PRT

<213> Homo sapiens

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Lys Lys Arg Arg Glu Arg Glu Arg Gln Asn Ile Val Leu Trp Arg
35 40 45

Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile 50 55 60

Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val 65 70 75 80

Ser Phe Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu
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Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu 100 105 110

Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly 115 120 125

Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser 130 135 140

Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro 145 150 155 160

Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly 165 170 175

Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys
180 185 190

Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met 195 200 205

Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr 210 215 220

Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe 225 230 235 240

Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly

245 250 255

Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp 260 265 270

Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe 275 280 285

Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln 290 295 300

Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met 305 310 315 320

Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys 325 330 335

Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys 340 345 350

Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe 355 360 365

Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile 370 375 380

Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn 385 390 395 400

Ser Glu Glu Lys Thr Lys

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<211> 1330

<212> DNA

<213> Homo sapiens

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<211> 245

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<213> Homo sapiens

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Glu Gln Ala Met Pro Gly Ala Gly Pro Gly Val Pro Gln Leu Gly Asn 35 40 45

Met Ala Val Ile His Ser His Leu Trp Lys Gly Leu Gln Glu Lys Phe 50 55 60

Leu Lys Gly Glu Pro Lys Val Leu Gly Val Val Gln Ile Leu Thr Ala 65 70 75 80

Leu Met Ser Leu Ser Met Gly Ile Thr Met Met Cys Met Ala Ser Asn 85 90 95

Thr Tyr Gly Ser Asn Pro Ile Ser Val Tyr Ile Gly Tyr Thr Ile Trp
100 105 110

Gly Ser Val Met Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala Ala Gly
115 120 125

Ile Arg Thr Thr Lys Gly Leu Val Arg Gly Ser Leu Gly Met Asn Ile 130 135 140

Thr Ser Ser Val Leu Ala Ala Ser Gly Ile Leu Ile Asn Thr Phe Ser 145 150 155 160

Leu Ala Phe Tyr Ser Phe His His Pro Tyr Cys Asn Tyr Tyr Gly Asn 165 170 175

Ser Asn Asn Cys His Gly Thr Met Ser Ile Leu Met Gly Leu Asp Gly 180 185 190

Met Val Leu Leu Ser Val Leu Glu Phe Cys Ile Ala Val Ser Leu 195 200 205

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Ala Glu Asn Phe Pro Phe Cys Thr Ile Asp Pro Asn Glu Ser Arg Val
Pro Val Pro Asp Glu Arg Phe Asp Phe Leu Cys Gln Tyr His Lys Pro
Ala Ser Lys Ile Pro Ala Phe Leu Asn Val Val Asp Ile Ala Gly Leu
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Val Lys Gly Ala His Asn Gly Gln Gly Leu Gly Asn Ala Phe Leu Ser

His Ile Ser Ala Cys Asp Gly Ile Phe His Leu Thr Arg Ala Phe Glu 115 120 125

- Asp Asp Asp Ile Thr His Val Glu Gly Ser Val Asp Pro Ile Arg Asp 130 135 140
- Ile Glu Ile Ile His Glu Glu Leu Gln Leu Lys Asp Glu Glu Met Ile 145 150 155 160
- Gly Pro Ile Ile Asp Lys Leu Glu Lys Val Ala Val Arg Gly Gly Asp 165 170 175
- Lys Lys Leu Lys Pro Glu Tyr Asp Ile Met Cys Lys Val Lys Ser Trp 180 185 190
- Val Ile Asp Gln Lys Thr Pro Val Arg Phe Tyr His Asp Trp Asn Asp 195 200 205
- Lys Glu Ile Glu Val Leu Asn Thr His Leu Phe Leu Thr Ser Lys Pro 210 215 220
- Met Val Tyr Leu Val Asn Leu Ser Glu Lys Asp Tyr Ile Arg Lys Lys 225 230 235 240
- Asn Lys Trp Leu Ile Lys Ile Lys Glu Trp Val Asp Lys Tyr Asp Pro 245 250 255
- Gly Ala Leu Val Ile Pro Phe Ser Gly Ala Leu Glu Leu Lys Leu Gln 260 265 270
- Glu Leu Ser Ala Glu Glu Arg Gln Lys Tyr Leu Glu Ala Asn Met Thr 275 280 285
- Gln Ser Ala Leu Pro Lys Ile Ile Lys Ala Gly Phe Ala Ala Leu Gln 290 295 300
- Leu Glu Tyr Phe Phe Thr Ala Gly Pro Asp Glu Val Arg Ala Trp Thr 305 310 315 320
- Ile Arg Lys Gly Thr Lys Ala Pro Gln Ala Ala Gly Lys Ile His Thr 325 330 335
- Asp Phe Glu Lys Gly Phe Ile Met Ala Glu Val Met Lys Tyr Glu Asp 340 345 350
- Phe Lys Glu Glu Gly Ser Glu Asn Ala Val Lys Ala Ala Gly Lys Tyr 355 360 365
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Asn Val Gly Thr Asp Leu Ser Pro Glu Pro Lys Ser Phe Asn Tyr Pro 115 120 125

Leu Leu Ser Ser Gln Val Ile Ser Leu Lys Phe Ser 130 135 140

International application No. PCT/US99/18298

IPC(6) US CL	SSIFICATION OF SUBJECT MATTER :Please See Extra Sheet. :Please See Extra Sheet. to International Patent Classification (IPC) or to both	h national classification and IPC	
<u>_</u>	DS SEARCHED		
Minimum d	ocumentation searched (classification system follows	ed by classification symbols)	
U.S. :	536/23.1, 23.5; 530/300, 350; 435/69.1, 320.1, 3	25, 252.3, 254.11; 514/2, 12	
Documental	tion searched other than minimum documentation to th	e extent that such documents are included	in the fields searched

Electronic d	lata base consulted during the international search (r	name of data base and, where practicable	e, search terms used)
WEST, I search ter	MEDLINE rms: co62?, kenneth jacobs		
с. рос	UMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where a	ppropriate, of the relevant passages	Relevant to claim No.
Х, Р	WO 98/45436 A2 (GENETICS INS 1998, especially SEQ ID NO: 407 on		1
x	Database Medline on Dialog, US Na (Bethesda, MD, USA) GenBank Ac NCI-CGAP http://www.ncbi.nlm.nih.ginstitute, Cancer Genome Anatomy P Index'. 13 August 1997.	ccession Number AA287697 gov/ncicgap. 'National Cancer	1-3
x	Database Medline on Dialog, US Na (Bethesda, MD, USA) GenBank Ac HILLIER et al. 'WashU-Merck EST I	cession Number AA179549.	1-3
x	Database Medline on Dialog, US Na (Bethesda, MD, USA) GenBank Ac HILLIER et al. 'Generation and analys sequence tags'. 02 February 1997.	cession Number AA057573.	1-3
X Furth	er documents are listed in the continuation of Box (C. See patent family annex.	
"A" doc	scial categories of cited documents: nument defining the general state of the art which is not considered	bT' later document published after the inte date and not in conflict with the appli the principle or theory underlying the	cation but cited to understand
	be of perticular relevance tier document published on or after the international filing data	*X* document of particular relevance; the	claimed invention cannot be
"L" doc	cument which may throw doubts on priority claim(s) or which is id to establish the publication date of another citation or other	considered novel or cannot be consider when the document is taken alone "Y" document of particular relevance; the	·
•	cial reason (as specified) nument referring to an oral disclosure, use, exhibition or other ans	considered to involve an inventive combined with one or more other such being obvious to a person skilled in the	step when the document is documents, such combination
	nument published prior to the internstional filing date but later than priority date claimed	*&* document member of the same patent	famîly
	actual completion of the international search MBER 1999	Date of mailing of the international sea 0 9 DEC 1999	rch report
Commission Box PCT	nailing address of the ISA/US ner of Patents and Trademarks b, D.C. 20231	Authorized officer CLAIRE M. KAUFMAN	5 rulages
Facsimile N	o. (703) 305-3230	Telephone No. (703) 308-0196	~\

International application No.
PCT/US99/18298

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No	
x	BOSSY et al. Conservation of neural nicotinic acetylcholine receptors from Drosophila to vertebrate central nervous systems. EMBO J. June 1988, Vol.7, No. 3, pages 611-618, especially Figure 2.		
X, P	Database Medline on Dialog, US National Library of Medicine, (Bethesda, MD, USA) GenBank Accession Number AL035661. SULSTON J. 'Direct Submission'. 15 March 1999.	1	
		,	

International application No. PCT/US99/18298

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
Please See Extra Sheet.
As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. X No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-11
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

International application No. PCT/US99/18298

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C07K 14/435, 14/00, 7/06; C12N 5/10, 15/10, 15/11, 15/12, 15/63; A61K 38/16

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

536/23.1, 23.5; 530/300, 350; 435/69.1, 320.1, 325, 252.3, 254.11; 514/2, 12

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group, I, claim(s)1-11, drawn to polynucleotide of clone co62_12, gene, vector, host cell, method of producing a protein and encoded protein.

Group II-LXXIX, each group consisting of two consecutive claims, drawn to polynucleotide of a distinct clone and encoded protein.

The inventions listed as Groups I-LXXIX do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I corresponds to the first invention wherein the first product is the polynucleotide and the first method of using is the method of making the protein. Note there is no method of making the polynucleotide. The invention also includes the protein made. Each group does not share the same or corresponding special technical feature because each group is drawn to a different polynucleotide and encoded protein. This Authority therefore considers that the several inventions do not share a special technical feature within the meaning of PCT Rule 13.2 and thus do not relate to a single general inventive concept within the meaning of PCT Rule 13.1.